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## **RAW SEQUENCE LISTING ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/435,257C  
 Source: 1600 (FJ/E)  
 Date Processed by STIC: 1/4/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENT IN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

## Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>09/435,257C</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1. <u>  </u> Wrapped Nucleics <u>  </u> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2. <u>  </u> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3. <input checked="" type="checkbox"/> Misaligned Amino <u>  </u> Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4. <input checked="" type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5. <u>  </u> Variable Length	Sequence(s) <u>      </u> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6. <u>  </u> PatentIn 2.0 <u>  </u> "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <u>      </u> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7. <u>  </u> Skipped Sequences (OLD RULES)	Sequence(s) <u>      </u> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8. <u>  </u> Skipped Sequences (NEW RULES)	Sequence(s) <u>      </u> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9. <u>  </u> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10. <u>  </u> Invalid <213> <u>  </u> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11. <u>  </u> Use of <220>	Sequence(s) <u>      </u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12. <u>  </u> PatentIn 2.0 <u>  </u> "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13. <u>  </u> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>	



IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/435,257C

DATE: 01/02/2004

TIME: 16:04:48

Input Set : A:\APBISeqList.txt

Output Set: N:\CRF4\01022004\I435257C.raw

4 <110> APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE  
6 <120> TITLE OF INVENTION: FK506-BASED REGULATION OF BIOLOGICAL EVENTS  
8 <130> FILE REFERENCE: APBI-P01-385  
10 <140> CURRENT APPLICATION NUMBER: 09/435,257C  
11 <141> CURRENT FILING DATE: 1999-11-05  
13 <150> PRIOR APPLICATION NUMBER: 60/107,473  
14 <151> PRIOR FILING DATE: 1998-11-06  
16 <160> NUMBER OF SEQ ID NOS: 35  
18 <170> SOFTWARE: PatentIn version 3.2

## ERRORED SEQUENCES

455 &lt;210&gt; SEQ ID NO: 33

456 &lt;211&gt; LENGTH: 514

457 &lt;212&gt; TYPE: PRT

458 &lt;213&gt; ORGANISM: Human

460 &lt;400&gt; SEQUENCE: 33

461 Met Ala Ala Pro Glu Pro Ala Arg Ala Ala Pro Pro Pro Pro Pro Pro  
E--> 462 Pro Pro Pro Pro Gly Ala Asp Arg Val Val Lys Ala Val Pro Phe  
E--> 463 Pro Pro Thr His Arg Leu Thr Ser Glu Glu Val Phe Asp Leu Asp Gly  
E--> 464 Ile Pro Arg Val Asp Val Leu Lys Asn His Leu Val Lys Glu Gly Arg  
E--> 465 Val Asp Glu Glu Ile Ala Leu Arg Ile Ile Asn Glu Gly Ala Ala Ile  
E--> 466 Leu Arg Arg Glu Lys Thr Met Ile Glu Val Glu Ala Pro Ile Thr Val  
E--> 467 Cys Gly Asp Ile His Gly Gln Phe Phe Asp Leu Met Lys Leu Phe Glu  
E--> 468 Val Gly Gly Ser Pro Ala Asn Thr Arg Tyr Leu Phe Leu Gly Asp Tyr  
E--> 469 Val Asp Arg Gly Tyr Phe Ser Ile Glu His Val Leu Gly Thr Glu Asp  
E--> 470 Ile Ser Ile Asn Pro His Asn Asn Ile Asn Glu Cys Val Leu Tyr Leu  
E--> 471 Trp Val Leu Lys Ile Leu Tyr Pro Ser Thr Leu Phe Leu Leu Leu Arg  
E--> 472 Gly Asn His Glu Cys Arg His Leu Thr Glu Tyr Phe Thr Phe Lys Gln  
E--> 473 Glu Cys Lys Ile Lys Tyr Ser Glu Arg Val Tyr Glu Ala Cys Met Glu  
E--> 474 Ala Phe Asp Ser Leu Pro Leu Ala Ala Leu Leu Asn Gln Gln Phe Leu  
E--> 475 Cys Val His Gly Gly Leu Ser Pro Glu Ile His Thr Leu Asp Asp Ile  
E--> 476 Arg Arg Leu Asp Arg Phe Lys Glu Pro Pro Ala Phe Gly Pro Met Cys  
E--> 477 Asp Leu Leu Trp Ser Asp Pro Ser Glu Asp Phe Gly Asn Glu Lys Ser  
E--> 478 Gln Glu His Phe Ser His Asn Thr Val Arg Gly Cys Ser Tyr Phe Tyr  
E--> 479 Asn Tyr Pro Ala Val Cys Glu Phe Leu Gln Asn Asn Asn Leu Leu Ser  
E--> 480 Ile Ile Arg Ala His Glu Ala Gln Asp Ala Gly Tyr Arg Met Tyr Arg  
E--> 481 Lys Ser Gln Thr Thr Gly Phe Pro Ser Leu Ile Thr Ile Phe Ser Ala  
E--> 482 Pro Asn Tyr Leu Asp Val Tyr Asn Asn Lys Ala Ala Val Leu Lys Tyr  
E--> 483 Glu Asn Asn Val Met Asn Ile Arg Gln Phe Asn Cys Ser Pro His Pro  
E--> 484 Tyr Trp Leu Pro Asn Phe Met Asp Val Phe Thr Trp Ser Leu Pro Phe  
E--> 485 Val Gly Glu Lys Val Thr Glu Met Leu Val Asn Val Leu Ser Ile Cys

pp 1-6  
Does Not Comply  
Corrected Diskette Needed

number  
the  
amino  
acids  
under every  
5 amino acids  
do not use  
TAB codes  
between the  
numbers. Use  
space characters.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/435,257C

DATE: 01/02/2004

TIME: 16:04:48

Input Set : A:\APBISeqList.txt

Output Set: N:\CRF4\01022004\1435257C.raw

E--> 486 Ser Asp Asp Glu Leu Met Thr Glu Gly Glu Asp Gln Phe Asp Gly Ser  
 E--> 487 Ala Ala Ala Arg Lys Glu Ile Ile Arg Asn Lys Ile Arg Ala Ile Gly  
 E--> 488 Lys Met Ala Arg Val Phe Ser Val Leu Arg Glu Glu Ser Glu Ser Val  
 E--> 489 Leu Thr Leu Lys Gly Leu Thr Pro Thr Gly Met Leu Pro Ser Gly Val  
 E--> 490 Leu Ala Gly Gly Arg Gln Thr Leu Gln Ser Gly Asn Asp Val Met Gln  
 E--> 491 Leu Ala Val Pro Gln Met Asp Trp Gly Thr Pro His Ser Phe Ala Asn  
 E--> 492 Asn Ser His Asn Ala Cys Arg Glu Phe Leu Leu Phe Phe Ser Ser Cys  
 E--> 493 Leu Ser Ser  
 547 <210> SEQ ID NO: 35  
 548 <211> LENGTH: 170  
 549 <212> TYPE: PRT  
 550 <213> ORGANISM: Human  
 552 <400> SEQUENCE: 35  
 553 Met Gly Asn Glu Ala Ser Tyr Pro Leu Glu Met Cys Ser His Phe Asp  
 E--> 554 1      ~~5~~ ~~10~~ ~~5~~ ~~15~~      10      15  
 555 Ala Asp Glu Ile Lys Arg Leu Gly Lys Arg Phe Lys Lys Leu Asp Leu  
 E--> 556 20      25      30  
 557 Asp Asn Ser Gly Ser Leu Ser Val Glu Glu Phe Met Ser Leu Pro Glu  
 E--> 558 35      40      45  
 559 Leu Gln Gln Asn Pro Leu Val Gln Arg Val Ile Asp Ile Phe Asp Thr  
 E--> 560 50      55      60  
 561 Asp Gly Asn Gly Glu Val Asp Phe Lys Glu Phe Ile Glu Gly Val Ser  
 E--> 562 65      70      75      80  
 563 Gln Phe Ser Val Lys Gly Asp Lys Glu Gln Lys Leu Arg Phe Ala Phe  
 E--> 564 85      90      95  
 565 Arg Ile Tyr Asp Met Asp Lys Asp Gly Tyr Ile Ser Asn Gly Glu Leu  
 E--> 566 100      105      110  
 567 Phe Gln Val Leu Lys Met Met Val Gly Asn Asn Leu Lys Asp Thr Gln  
 E--> 568 115      120      125  
 569 Leu Gln Gln Ile Val Asp Lys Thr Ile Ile Asn Ala Asp Lys Asp Gly  
 E--> 570 130      135      140  
 571 Asp Gly Arg Ile Ser Phe Glu Glu Phe Cys Ala Val Val Gly Gly Leu  
 E--> 572 145      150      155      160  
 573 Asp Ile His Lys Lys Met Val Val Asp Val  
 E--> 574 165      170

number the  
 amino acids  
 under every  
 5 amino  
 acids

misaligned  
 numbers

(see item 3  
 on Error  
 Summary  
 sheet)

see following pages  
 for more errors

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/435,257C

DATE: 01/02/2004  
TIME: 16:04:49

Input Set : A:\APBISegList.txt  
Output Set: N:\CRF4\01022004\I435257C.raw

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:1

see p. 4 for example

09/455,257C.4

<210> 1  
<211> 14  
<212> PRT  
<213> Artificial Sequence

needs 2207-2237 explanation

&lt;400&gt; 1

Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg  
1 5 10

## VARIABLE LOCATION SUMMARY

DATE: 01/02/2004

PATENT APPLICATION: US/09/435,257C

TIME: 16:04:49

Input Set : A:\APBISegList.txt

Output Set: N:\CRF4\01022004\I435257C.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of &lt;220&gt; to &lt;223&gt; is MANDATORY if n's or Xaa's are present.

in &lt;220&gt; to &lt;223&gt; section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:28; N Pos. 33,34,36,37,45,46

Seq#:31; N Pos. 32,33,35,36

*see p.6 for example*



09/435,257C

6

<210> 28  
<211> 64  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide

<400> 28  
gctgtaactg tgtatctttc agattgttcc c<sup>nn</sup>nn<sup>nn</sup>cat ctt<sup>nn</sup>nn<sup>nn</sup>tacc tggaagagtt  
cccc

60  
64

n/s

need explanation in 2207-2237  
section

same error in sequence 31

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## VERIFICATION SUMMARY

DATE: 01/02/2004

PATENT APPLICATION: US/09/435,257C

TIME: 16:04:49

Input Set : A:\APBISeqList.txt

Output Set: N:\CRF4\01022004\I435257C.raw

L:25 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:1, <213>  
ORGANISM:Artificial Sequence

L:25 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>  
ORGANISM:Artificial Sequence

L:25 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:25

L:365 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:28

L:365 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:28

L:365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0

L:403 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:31

L:403 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:31

L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0

L:462 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:33

M:332 Repeated in SeqNo=33

L:493 M:252 E: No. of Seq. differs, <211> LENGTH:Input:514 Found:515 SEQ:33

L:554 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35

M:332 Repeated in SeqNo=35